

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/835,107

DATE: 09/06/2001

TIME: 15:59:23

Input Set : A:\sequence listing.txt

Output Set: N:\CRF3\09062001\I835107.raw

ENTERED

4 <110> APPLICANT: Tudan, Christopher R.
 5 Merzouk, Ahmed
 6 Arab, Lakhdar
 7 Saxena, Geeta
 8 Eaves, Connie J.
 9 Cashman, Johanne
 10 Clark-Lewis
 11 Salari, Hassan
 14 <120> TITLE OF INVENTION: CXCR4 AGONIST TREATMENT OF HEMATOPOIETIC CELLS
 18 <130> FILE REFERENCE: SMAR012
 21 <140> CURRENT APPLICATION NUMBER: US 09/835,107
 C--> 23 <141> CURRENT FILING DATE: 2001-08-20
 27 <150> PRIOR APPLICATION NUMBER: CA 2,305,036
 29 <151> PRIOR FILING DATE: 2000-04-12
 33 <150> PRIOR APPLICATION NUMBER: US 60/232,425
 35 <151> PRIOR FILING DATE: 2000-09-14
 39 <150> PRIOR APPLICATION NUMBER: CA 2,335,109
 41 <151> PRIOR FILING DATE: 2001-02-23
 45 <160> NUMBER OF SEQ ID NOS: 34
 49 <170> SOFTWARE: PatentIn Ver. 2.0
 53 <210> SEQ ID NO: 1
 55 <211> LENGTH: 67
 57 <212> TYPE: PRT
 59 <213> ORGANISM: Homo sapiens
 63 <220> FEATURE:
 65 <223> OTHER INFORMATION: SDF-1 alpha
 69 <400> SEQUENCE: 1
 71 Lys Pro Val Ser Leu Ser Tyr Arg Cys Pro Cys Arg Phe Phe Glu Ser
 73 1 5 10 15
 77 His Val Ala Arg Ala Asn Val Lys His Leu Lys Ile Leu Asn Thr Pro
 79 20 25 30
 83 Asn Cys Ala Leu Gln Ile Val Ala Arg Leu Lys Asn Asn Asn Arg Gln
 85 35 40 45
 89 Val Cys Ile Asp Pro Lys Leu Lys Trp Ile Gln Glu Tyr Leu Glu Lys
 91 50 55 60
 95 Ala Leu Asn
 97 65
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 105 <211> LENGTH: 93
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 109 <213> ORGANISM: Homo sapiens
 113 <220> FEATURE:
 115 <223> OTHER INFORMATION: SDF-1 Precursor, PBSF
 119 <400> SEQUENCE: 2
 121 Met Asn Ala Lys Val Val Val Val Leu Val Leu Val Leu Thr Ala Leu
 123 1 5 10 15
 127 Cys Leu Ser Asp Gly Lys Pro Val Ser Leu Ser Tyr Arg Cys Pro Cys

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129          20          25          30
133 Arg Phe Phe Glu Ser His Val Ala Arg Ala Asn Val Lys His Leu Lys
135          35          40          45
139 Ile Leu Asn Thr Pro Asn Cys Ala Leu Gln Ile Val Ala Arg Leu Lys
141          50          55          60
145 Asn Asn Asn Arg Gln Val Cys Ile Asp Pro Lys Leu Lys Trp Ile Gln
147 65          70          75          80
151 Glu Tyr Leu Glu Lys Ala Leu Asn Lys Arg Phe Lys Met
153          85          90
159 <210> SEQ ID NO: 3
161 <211> LENGTH: 93
163 <212> TYPE: PRT
165 <213> ORGANISM: Homo sapiens
169 <220> FEATURE:
171 <223> OTHER INFORMATION: SDF-1 beta
175 <400> SEQUENCE: 3
177 Met Asn Ala Lys Val Val Val Val Leu Val Leu Val Leu Thr Ala Leu
179 1          5          10          15
183 Cys Leu Ser Asp Gly Lys Pro Val Ser Leu Ser Tyr Arg Cys Pro Cys
185          20          25          30
189 Arg Phe Phe Glu Ser His Val Ala Arg Ala Asn Val Lys His Leu Lys
191          35          40          45
195 Ile Leu Asn Thr Pro Asn Cys Ala Leu Gln Ile Val Ala Arg Leu Lys
197          50          55          60
201 Asn Asn Asn Arg Gln Val Cys Ile Asp Pro Lys Leu Lys Trp Ile Gln
203 65          70          75          80
207 Glu Tyr Leu Glu Lys Ala Leu Asn Lys Arg Phe Lys Met
209          85          90
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217 <211> LENGTH: 17
219 <212> TYPE: PRT
221 <213> ORGANISM: Artificial Sequence
225 <220> FEATURE:
227 <223> OTHER INFORMATION: Synthesised in Laboratory: SDF-1(1-17): or
229 CTCE9902
233 <400> SEQUENCE: 4
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237 1          5          10          15
241 His
249 <210> SEQ ID NO: 5
251 <211> LENGTH: 6
253 <212> TYPE: PRT
255 <213> ORGANISM: Artificial Sequence
259 <220> FEATURE:
261 <223> OTHER INFORMATION: Synthesised in Laboratory
265 <400> SEQUENCE: 5
267 Arg Phe Phe Glu Ser His
269 1          5
275 <210> SEQ ID NO: 6

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277 <211> LENGTH: 9
 279 <212> TYPE: PRT
 281 <213> ORGANISM: Artificial Sequence
 285 <220> FEATURE:
 287 <223> OTHER INFORMATION: Synthesised in Laboratory
 291 <400> SEQUENCE: 6
 293 Lys Pro Val Ser Leu Ser Tyr Arg Cys
 295 1 5
 301 <210> SEQ ID NO: 7
 303 <211> LENGTH: 9
 305 <212> TYPE: PRT
 307 <213> ORGANISM: Artificial Sequence
 311 <220> FEATURE:
 313 <221> NAME/KEY: DISULFID
 315 <222> LOCATION: (9)
 317 <223> OTHER INFORMATION: Disulphide linkage between each cys at position 9
 319 of each monomer.
 323 <220> FEATURE:
 325 <223> OTHER INFORMATION: Synthesised in Laboratory:
 327 SDF-1(1-9)2-C9/C9-cysteine dimer: or CTCE9901
 331 <400> SEQUENCE: 7
 333 Lys Pro Val Ser Leu Ser Tyr Arg Cys
 335 1 5
 341 <210> SEQ ID NO: 8
 343 <211> LENGTH: 10
 345 <212> TYPE: PRT
 347 <213> ORGANISM: Artificial Sequence
 351 <220> FEATURE:
 353 <221> NAME/KEY: MUTAGEN
 355 <222> LOCATION: (10)
 357 <223> OTHER INFORMATION: Xaa may be lysine with both the alpha and the
 359 epsilon amino groups of the lysine being
 361 associated with the covalent (amide) bond
 363 formation.
 367 <220> FEATURE:
 369 <223> OTHER INFORMATION: Synthesised in Laboratory
 373 <220> FEATURE:
 375 <221> NAME/KEY: VARIANT
 377 <222> LOCATION: (10)
 379 <223> OTHER INFORMATION: Xaa = a linking moiety between each of the cys at
 381 pos. 9 in each SEQ ID Nos: 8 and 9
 385 <400> SEQUENCE: 8
 387 Lys Pro Val Ser Leu Ser Tyr Arg Cys Xaa
 389 1 5 10
 395 <210> SEQ ID NO: 9
 397 <211> LENGTH: 9
 399 <212> TYPE: PRT
 401 <213> ORGANISM: Artificial Sequence
 405 <220> FEATURE:

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407 <223> OTHER INFORMATION: Synthesised in Laboratory
 411 <400> SEQUENCE: 9
 413 Lys Pro Val Ser Leu Ser Tyr Arg Cys
 415 1 5
 421 <210> SEQ ID NO: 10
 423 <211> LENGTH: 9
 425 <212> TYPE: PRT
 427 <213> ORGANISM: Artificial Sequence
 431 <220> FEATURE:
 433 <221> NAME/KEY: MUTAGEN
 435 <222> LOCATION: (9)
 437 <223> OTHER INFORMATION: Xaa may be lysine with both the alpha and the
 439 epsilon amino groups of the lysine being
 441 associated with the covalent (amide) bond
 443 formation.
 447 <220> FEATURE:
 449 <223> OTHER INFORMATION: Synthesised in Laboratory
 453 <220> FEATURE:
 455 <221> NAME/KEY: VARIANT
 457 <222> LOCATION: (9)
 459 <223> OTHER INFORMATION: Xaa = a linking moiety between each of the arg at
 461 pos. 8 in each SEQ ID Nos: 10 and 11
 465 <400> SEQUENCE: 10
 467 Lys Pro Val Ser Leu Ser Tyr Arg Xaa
 469 1 5
 475 <210> SEQ ID NO: 11
 477 <211> LENGTH: 8
 479 <212> TYPE: PRT
 481 <213> ORGANISM: Artificial Sequence
 485 <220> FEATURE:
 487 <223> OTHER INFORMATION: Synthesised in Laboratory
 491 <400> SEQUENCE: 11
 493 Lys Pro Val Ser Leu Ser Tyr Arg
 495 1 5
 501 <210> SEQ ID NO: 12
 503 <211> LENGTH: 30
 505 <212> TYPE: PRT
 507 <213> ORGANISM: Artificial Sequence
 511 <220> FEATURE:
 513 <221> NAME/KEY: DOMAIN
 515 <222> LOCATION: (15)..(17)
 517 <223> OTHER INFORMATION: spacer monomers (such as the illustrated glycine
 519 G's) may be used in variable numbers, such as 2, 3
 521 or 4 glycines.
 525 <220> FEATURE:
 527 <223> OTHER INFORMATION: Synthesised in Laboratory:
 529 SDF-1(1-14)-(G)3-SDF-1(55-67) acid
 533 <400> SEQUENCE: 12
 535 Lys Pro Val Ser Leu Ser Tyr Arg Cys Pro Cys Arg Phe Phe Gly Gly

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537      1              5              10              15
541 Gly Leu Lys Trp Ile Gln Glu Tyr Leu Glu Lys Ala Leu Asn
543              20              25              30
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553 <212> TYPE: PRT
555 <213> ORGANISM: Artificial Sequence
559 <220> FEATURE:
561 <221> NAME/KEY: DOMAIN
563 <222> LOCATION: (16)..(19)
565 <223> OTHER INFORMATION: spacer monomers (such as the illustrated glycine
567      G's) may be used in variable numbers, such as 2, 3
569      or 4 glycines.
573 <220> FEATURE:
575 <223> OTHER INFORMATION: Synthesised in Laboratory:
577      SDF-1(1-14)-(G)4-SDF-1(55-67) acid: or CTCE0013
581 <400> SEQUENCE: 13
583 Lys Pro Val Ser Leu Ser Tyr Arg Cys Pro Cys Arg Phe Phe Gly Gly
585      1              5              10              15
589 Gly Gly Leu Lys Trp Ile Gln Glu Tyr Leu Glu Lys Ala Leu Asn
591              20              25              30
597 <210> SEQ ID NO: 14
599 <211> LENGTH: 30
601 <212> TYPE: PRT
603 <213> ORGANISM: Artificial Sequence
607 <220> FEATURE:
609 <221> NAME/KEY: DOMAIN
611 <222> LOCATION: (15)..(17)
613 <223> OTHER INFORMATION: spacer monomers (such as the illustrated glycine
615      G's) may be used in variable numbers, such as 2, 3
617      or 4 glycines.
621 <220> FEATURE:
623 <223> OTHER INFORMATION: Synthesised in Laboratory:
625      SDF-1(1-14)-(G)3-SDF-1(55-67) amide
629 <220> FEATURE:
631 <221> NAME/KEY: MOD_RES
633 <222> LOCATION: (30)
635 <223> OTHER INFORMATION: AMIDATION
639 <400> SEQUENCE: 14
641 Lys Pro Val Ser Leu Ser Tyr Arg Cys Pro Cys Arg Phe Phe Gly Gly
643      1              5              10              15
647 Gly Leu Lys Trp Ile Gln Glu Tyr Leu Glu Lys Ala Leu Asn
649              20              25              30
655 <210> SEQ ID NO: 15
657 <211> LENGTH: 31
659 <212> TYPE: PRT
661 <213> ORGANISM: Artificial Sequence
665 <220> FEATURE:
667 <221> NAME/KEY: DOMAIN

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/835,107

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Input Set : A:\sequence listing.txt

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L:23 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:387 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8

L:467 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10